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Box PATENT APPLICATION

Assistant Commissioner for Patents

Washington, D.C. 20231

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Sir:

Transmitted herewith for filing is a patent application of Inventors: Kan-Hung Lee, Chi-Horng Bair, Yang-Yuan Tseng, Yih-Weng Wang and Shin-Hwan Wang

For: METHOD FOR DETECTING AND DIFFERENTIATING
ENTEROVIRUSES AND THE PRIMERS AND PROBES THEREFOR

Enclosed are also:

- ☒ 1 sheet of drawings.
- ☒ Disk containing sequence listing.
- ☒ Declaration/Power of Attorney form.
- ☒ Assignment.
- ☒ Verified Statement Claiming Small Entity Status.

Claims as Filed
SMALL ENTITY

For	Number Filed	Number Extra	Rate	Basic Fee \$ 355.00
Total Claims	26-20	06	\$09.00	= \$ 54.00
Independent Claims	02-03	0	\$40.00	= \$ 000.00
Total Filing Fee-----				\$ 409.00

- ☒ A check in the amount of \$449.00 to cover the filing fee and recording fee is enclosed.

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Jan E. Sands
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INSTRUCTIONS

SMALL BUSINESS

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NAME OF CONCERN: DR. Chip Biotechnology Incorporation

ADDRESS OF CONCERN: No. 621, Sec. 4, Wen Hsin Rd., Taichung City, Taiwan, R.O.C.

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

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I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled Method for Detecting and Differentiating Enteroviruses and the Primers and Probes Therefor by inventor(s) Kan-Hung LEE, Chi-Horng BAIR, Yang-Yuan TSENG, Yih-Weng WANG & Shin-Hwan WANG described in

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Insert

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Sign. date

SIGNATURE Yang Wen-TungDATE November 22, 2000

METHODS FOR DETECTING AND DIFFERENTIATING
ENTEROVIRUSES AND THE PRIMERS AND PROBES
THEREFOR

Background of the Invention

5 Enteroviruses belong to the family *Picornaviridae* that represents a very large RNA-virus family with respect to the number of members but one of the smallest in terms of virion size and complexity. The virion of an enterovirus consists of a capsid of 60 subunits. Each subunit consisting of the four proteins (VP1-VP4) arranged with icosahedral symmetry around a
10 genome made up of a single strand of positive-sense RNA. Enteroviruses are transient inhabitants of the human alimentary tract and may be isolated from the lower intestine or the throat. Enteroviruses of human origin include polioviruses (serotypes 1 to 3), coxsackieviruses of groups A (CAV, serotypes 1 to 22 and 24) and B (CBV, serotypes 1 to 6), echoviruses
15 (serotypes 1 to 9, 11 to 27 and 29 to 33) and enteroviruses (serotypes 68-71). Enteroviral infections in humans may result in a wide range of acute symptoms involving neurological, skin and mucosa, cardiac and muscular, ocular, respiratory and gastrointestinal conditions, as well as undifferentiated febrile illness, generalized diseases of infants and diabetes mellitus. Among
20 the nonpolio enteroviruses, some unclassified serotypes have been particularly prevalent in some countries and areas during summer and early fall, e.g., enteroviruses 70 and 71. Enterovirus 71 has been isolated from patients with meningitis, encephalitis and paralysis resembling poliomyelitis. It continues to be one of the main causes of central nervous system diseases,
25 sometimes fetal, around the world. Furthermore, the virus has caused outbreaks of human hand-foot-and-mouth disease in some areas, e.g., Japan, Sweden and Taiwan.

 Common diagnoses of enteroviruses usually include recovery of the virus and serological tests. The recovery of the virus may includes isolation
30 of the viruses from throat washings, throat swabs, stools, rectal swabs and

sometimes cerebrospinal fluid (in aseptic meningitis cases). The isolated viral specimens are inoculated into tissue cultures or suckling mice (the latter is specific for coxsackieviruses) for propagation and identification. It takes one to two weeks to complete a run of viral recovery. In addition,
5 intervention has to be made by qualified technicians.

Serologic tests are generally conducted by means of neutralization assays detecting the neutralizing antibodies specific to the infecting virus when they exist. For some echoviruses, hemagglutination-inhibition assays might show type-specific infections. Serum antibodies can also be detected
10 or titrated by the immunofluorescence technique using infected cell cultures on coverslips as antigens. However, serologic tests are difficult to evaluate because of the multiplicity of serotypes, unless the antigen used has been isolated from a specific human or during an epidemic outbreak of typical clinic illness. In all of the serologic assays, skilled artisans are required to
15 judge the cut-off values from the readouts. Also, a period of time and specialized techniques are usually required to prepare such an antigen used in those assays to reduce the incidence of heterotypic reactions or cross-reactions.

Neither the recovery of the virus nor the serologic tests provides a rapid
20 diagnostic tool. Nevertheless, the acute syndromes associated with enteroviruses may progress fast, and in some cases may even become fatal in a couple of days. There is therefore a need for a method to rapidly detect enteroviruses with ease in practice.

Summary of the Invention

25 The present invention relates to novel pairs of oligonucleotide primers for use in detecting the presence or absence of an enterovirus in a sample. Each pair of primers according to the present invention consists of a first primer and a second primer, which are useful in rapidly diagnosing the diseases or conditions associated with enteroviruses by nucleic acid
30 amplification assays, such as polymerase chain reactions.

It is surprisingly found in the present invention that some nucleotide

sequences correspond to the conserved portions in the nucleic acids of the enteroviruses. Therefore, the present invention further provides synthetic nucleotide sequences capable of specifically hybridizing to a sense strand of an enterovirus nucleic acid or a nucleic acid corresponding to the sense strand, such as the product of an amplification reaction with the sense strand as the template.

In another aspect, the present invention relates to a method of detecting the presence or absence of an enterovirus nucleic acid in a sample. The method according to the present invention comprises (a) contacting the sample with a pair of oligonucleotide primers according to the present invention in an amplification process; and (b) determining the presence or absence of an enterovirus by detecting the presence or absence of amplification products.

Preferably, in the method according to the present invention, the sample may be simultaneously contacted with a second pair of oligonucleotide primers according to the present invention in an amplification process in addition to the first pair of primers. The primers in the second pair are not the same as the primers in first pair. The primers in the second pair may have either the first or the second primer different from the corresponding primer in the first pair. Preferably, both primers in the second pair are different from the ones in the first pair. Furthermore, the sample may be simultaneously contacted with a third pair of the oligonucleotide primers according to the present invention in an amplification process, in addition to the first and second pairs of primers. In a similar manner, the third pair of primers is neither the same as the first pair of primers nor the second pair of primers.

In an alternative manner, the method according to the present invention may further comprise contacting the products of step (a) with a second pair of the oligonucleotide primers according to the present invention in an amplification process. The second pair of primers is chosen so as to be capable of being used to amplify a sequence in an amplification process that is equal to or within the sequence obtainable in the amplification process

using the first pair of primers.

In another alternative of the method according to present invention, the amplification products detected in step (b) are further subjected to a specific hybridization with at least one synthetic nucleotide sequence according to the present invention.

In yet another aspect, the present invention relates to a method of detecting and differentiating enterovirus type 71 in a sample. The method comprises (a) contacting the sample with at least one pair of oligonucleotide primers according to the present invention in an amplification process; (b) determining the presence or absence of enterovirus type 71 by detecting for the presence or absence of amplification products; and (c) subjecting the amplification products detected to a specific hybridization with at least one synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13. Preferably, the amplification products detected are subjected to a specific hybridization with the synthetic nucleotide sequences comprising the sequences of SEQ ID NO:12 and SEQ ID NO:13.

In yet another aspect, the present invention relates to a method of detecting and differentiating coxsackievirus A16 in a sample. The method comprises contacting the sample with a pair of oligonucleotide primers according to the present invention in an amplification process; determining the presence or absence of coxsackievirus A16 by detecting the presence or absence of amplification products; and subjecting the amplification products detected to a specific hybridization with at least one synthetic nucleotide sequence comprising the sequence of SEQ ID NO:14 or SEQ ID NO:15. Preferably, the amplification products detected are subjected to a specific hybridization with the synthetic nucleotide sequences comprising the sequences of SEQ ID NO:14 and SEQ ID NO:15.

In yet another aspect, the present invention relates to a method of detecting and differentiating enterovirus type 71 and/or coxsackievirus A16 in a sample. The method comprises contacting the sample with a pair of oligonucleotide primers according to the present invention in an

amplification process; determining the presence or absence of enterovirus type 71 and/or coxsackievirus A16 by detecting the presence or absence of amplification products; and subjecting the amplification products detected to a specific hybridization with at least a first synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13, and with at least a second synthetic nucleotide sequence comprising the sequence of SEQ ID NO:14 or SEQ ID NO:15. Preferably, the amplification products detected are subjected to a specific hybridization with the synthetic nucleotide sequences comprising the sequences of SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14 and SEQ ID NO:15.

In yet another aspect, the present invention provides a kit for detecting an enterovirus in a sample, which comprises at least one pair of oligonucleotide primers according to the present invention. Preferably, the kit according to the present invention comprises more than one pair of primers according to the present invention. In an alternative of the present invention, the kit may further comprise at least one synthetic nucleotide sequence according to the present invention.

In yet another aspect, the present invention provides a kit for detecting and differentiating enterovirus type 71 in a sample, which comprises at least one pair of oligonucleotide primers according to the present invention and at least one synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13. Preferably, the kit according to the present invention comprises more than one pair of primers according to the present invention. In a preferred embodiment of this invention, the kit comprises the synthetic nucleotide sequences comprising the sequences of SEQ ID NO:12 and SEQ ID NO:13.

In yet another aspect, the present invention provides a kit for detecting and differentiating coxsackievirus A16 in a sample, which comprises at least one pair of oligonucleotide primers according to the present invention and at least one synthetic nucleotide sequence comprising the sequence of SEQ ID NO:14 or SEQ ID NO:15. Preferably, the kit according to the present

invention comprises more than one pair of primers according to the present invention. In a preferred embodiment of this invention, the kit comprises the synthetic nucleotide sequences comprising the sequences of SEQ ID NO:14 and SEQ ID NO:15.

5 In yet another aspect, the present invention provides a kit for detecting and differentiating enterovirus type 71 and/or coxsackievirus A16 in a sample, which comprises at least one pair of oligonucleotide primers according to the present invention; and at least a first synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13 and
10 at least a second synthetic nucleotide sequence comprising the sequence of SEQ ID NO:14 or SEQ ID NO:15. Preferably, the kit according to the present invention comprises more than one pair of primers according to the present invention. In a preferred embodiment of this invention, the kit comprises the synthetic nucleotide sequences comprising the sequences of
15 SEQ ID NOs:12-15.

Brief Description of the Figure

Figure 1 is a schematic representation showing a portion of cDNA sequence corresponding to the genome of enterovirus type 71, where the cDNA sequence with the Accession No. U22521 was obtained from the
20 database GenBank. The sequences in the boxes correspond to the primers and probes of the present invention that are identified with their codes designated by the inventors.

Detailed Description of the Preferred Embodiments

25 The term "specifically hybridizing" or "specific hybridization" means complementary hybridization between an oligonucleotide and a target sequence. The term "specific" or "specifically" refers to the specificity shown by the complementary hybridization, which allows for minor mismatches between the oligonucleotide and the sequence that may not jeopardize the annealing for detection of hybridization signals.

30 The term "sample" means a sample comprising any biological material

containing nucleic acids. Preferably the term "sample" refers to a biological sample including whole blood, serum, urine, saliva, cerebrospinal fluid, semen, tears, throat swab, rectal swab, feces and the like.

5 The term "amplification process" means an assay or method for amplifying a nucleic acid sequence. For instance, the "amplification process" includes a polymerase chain reaction (PCR) assay, a ligase chain reaction (LCR) assay, Q β -replicase amplification, *in vitro* transcription, *in vitro* retro-transcription and self-sustained sequence replication.

10 The term "highly stringent conditions" means the conditions of hybridization that are chosen to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The thermal melting point is the temperature (under the defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically, highly stringent conditions will be those in which
15 the salt concentration is about 0.2 molar at pH 7 and the temperature is at least above 60°C.

The codes for bases as used herein cover those representing naturally occurring purines and pyrimidines found in native DNA molecules (i.e., A, G, T and C), as well as those for mixed bases as usually recognized by persons
20 skilled in the art for syntheses of oligonucleotides (such as R, Y, S, H). With respect to the codes used in the present specification, A (or a) represents adenine, G (or g) represents guanine, T (or t) represents thymine, C (or c) represents cytosine, R (or r) represents either adenine or guanine, Y (or y) represents either cytosine or thymine, S (or s) represents either guanine or
25 cytosine, and H (or h) represents any of adenine, thymine and cytosine.

The present invention is useful for the detection of nucleic acids derived from enteroviruses. The present invention provides a rapid and sensitive method to detect the presence or absence of the nucleic acids derived from enteroviruses. In a preferred embodiment of the present invention, the
30 method according to the present invention is an assay on the basis of polymerase chain reactions (PCR). In another aspect, the present invention

provides very specific pairs of PCR primers that can be used to detect and/or identify particular serotypes of enteroviruses, such as enterovirus type 71 and coxsackievirus A16. In yet another aspect, the present invention provides specific nucleotide sequences, which are capable of specifically hybridizing with the nucleic acid fragments obtainable from the amplification process using the pairs of primers according to the present invention.

A number of amplification processes may be used, but a PCR-based process is preferred. The PCR process is well known in the art and is thus only briefly described herein. For a review of PCR methods and protocols, see, e.g., U.S. Patent Nos. 4,683,195 and 4,683,202; 4,965,188; and Innis, *et al.*, eds. PCR Protocols. "A Guide to Methods and Application" (Academic Press, Inc., San Diego, CA. 1990). PCR reagents and protocols are also commercially available.

Because enteroviruses are RNA viruses, the first step in the amplification is the synthesis of a DNA copy (cDNA) of the region to be amplified. Reverse transcription can be carried out as a separate step, or in a homogeneous reverse transcription-polymerase chain reaction (RT-PCR), a modification of the polymerase chain reaction for amplifying RNA. Methods suitable for PCR amplification of enterovirus nucleic acids are described in Romero and Rotbart in "Diagnostic Molecular Biology: Principles and Applications" pp.401-406, Persing *et al.* eds., (Mayo Foundation, Rochester, MN 1993); Rotbart et al. U.S. Patent No. 5,075,212 and Egger *et al.*, J. Clin. Microbiol. 33:1442-1447 (1995)).

The present invention provides novel pairs of oligonucleotide primers for use in detecting the presence or absence of enterovirus in a sample. Each pair of primers according to the present invention consists of a first primer and a second primer which are useful in diagnosing rapidly the diseases or conditions associated with enteroviruses by nucleic acid amplification assays, such as polymerase chain reactions. The primers according to the present invention target the sense or antisense strands of nucleotide sequences that correspond to particular conserved regions. Particular combinations of a

primer pair or groups of primer pairs yield a matrix of amplification products that is used to detect enteroviruses present in a sample. In the preferred combinations of the present invention, the first primer comprises a sequence selected from the group consisting of

- f1:** TTGTRCGCCTGTTTTA (SEQ ID NO: 1),
- f2:** CAAGCACTTCTGTHHCCCCGG (SEQ ID NO: 2),
- f3:** TACTTCGAGAARCCYAGTA (SEQ ID NO: 3),
- f5:** AAGAGYCTATTGAGCTA (SEQ ID NO: 4) and
- f7:** GGI TGG TRS TGG AAR TTI CC (SEQ ID NO: 5).

The second primer comprises a sequence selected from the group consisting of

- r1:** CACYGGATGGCCAATCCAA (SEQ ID NO: 6),
- r2:** ATTGTCACCATAAGCAGCCA (SEQ ID NO: 7), and
- r4:** AR RTT IAT CCA YTG RTG IGG (SEQ ID NO: 8).

The sequences of the primers of the present invention correspond to the known enteroviral cDNA sequences in the boxes as shown in Figure 1. When designing the primers, base modifications were made to the corresponding viral cDNA sequences so as to enhance the efficiency of primer annealing and broaden the spectrum of sequence diversity that the primers can be employed to detect.

The primers comprising the sequences of SEQ ID NOs: 5 and 8 according to the present invention correspond to the coding regions of the enteroviral genome. The primers corresponding to the coding regions of the enteroviral genome are intended to cover those primers comprising the degenerate sequences in relation to the sequences of SEQ ID NOs: 5 and 8. The sequences of SEQ ID NOs: 5 and 8 above are schematically depicted in relevant triplets according to the codons to which the sequences correspond.

In the present invention, a more preferred combination comprises one or more of the following primer pairs:

f1(SEQ ID NO: 1)/r1(SEQ ID NO: 6); f2(SEQ ID NO: 2)/r1(SEQ ID NO: 6);
f3(SEQ ID NO: 3)/r1(SEQ ID NO: 6); f5(SEQ ID NO: 4)/r1(SEQ ID NO: 6);
f1(SEQ ID NO: 1)/r2(SEQ ID NO: 7); f2(SEQ ID NO: 2)/r2(SEQ ID NO: 7);
f3(SEQ ID NO: 3)/r2(SEQ ID NO: 7); f5(SEQ ID NO: 4)/r2(SEQ ID NO: 7); and
f7(SEQ ID NO: 5)/r2(SEQ ID NO: 7).

In a preferred aspect of the present invention, the pair of primers f7(SEQ ID NO: 5)/r4(SEQ ID NO: 8) are particularly suited to the detection of enterovirus type 71 (EV71) and coxsackievirus A16 (Cox A 16) in an amplification process.

In view of Figure 1, persons skilled in the art can understand the way to choose at least a pair of primers of the present invention that are suitable for detecting and/or amplifying a desired fragment(s) in the enteroviral genome, and accordingly determine the pair(s) of primers with ease. As shown in Figure 1, the second primer should comprise the sequence of SEQ ID NO: 8 or a degenerate sequence thereof when the first primer comprises the sequence of SEQ ID NO: 5 or a degenerate sequence thereof.

To amplify a target nucleic acid sequence in a sample by PCR, the sequence must be accessible to the components of the amplification system. In general, this accessibility is ensured by isolating the nucleic acids from the sample. A variety of techniques for extracting nucleic acids, in particular ribonucleic acids, from biological samples are known in the art. Alternatively, if the sample is fairly readily disruptable, the nucleic acid need not be purified prior to amplification by the PCR technique, i.e., if the sample is comprised of cells, particularly peripheral blood lymphocytes or monocytes, lysis and dispersion of the intracellular components may be accomplished merely by suspending the cells in a hypotonic buffer.

The first step of each cycle of the PCR involves the separation of the nucleic acid duplex formed by the primer extension. Once the strands are separated, the next step in PCR involves hybridizing the separated strands with primers that flank the target sequence. The primers are then extended to form complementary copies of the target strands. For successful PCR

amplification, the primers are designed so that the position at which each primer hybridizes along a duplex sequence is such that an extension product synthesized from one primer, when separated from the template (complement), serves as a template for the extension of the other primer. The cycle of denaturation, hybridization, and extension is repeated as many times as necessary to obtain the desired amount of amplified nucleic acid.

In the preferred embodiment of the PCR process, strand separation is achieved by heating the reaction to a sufficiently high temperature for a sufficient time to cause the denaturation of the duplex but not to cause an irreversible denaturation of the polymerase (see U.S. Patent No. 4,965,188). Template-dependent extension of primers in PCR is catalyzed by a polymerizing agent in the presence of adequate amounts of four deoxyribonucleoside triphosphates (typically dATP, dGTP, dCTP, and dTTP) in a reaction medium comprised of the appropriate salts, metal cations, and pH buffering system. Suitable polymerizing agents are enzymes known to catalyze template-dependent DNA synthesis. In the present invention, the initial template for primer extension is typically RNA. Reverse transcriptases (RTs) suitable for synthesizing a cDNA from the RNA template are well known.

PCR is most usually carried out as an automated process with a thermostable enzyme. In this process, the temperature of the reaction mixture is cycled through a denaturing region, a primer annealing region and an extension reaction region automatically.

As described above, a preferred embodiment of the invention incorporates RT-PCR amplification. A person skilled in the art will recognize, however, that amplification of target sequences in a sample may be accomplished by any known method, such as ligase chain reaction (LCR), Q β -replicase amplification, *in vitro* transcription, and self-sustained sequence replication, each of which provides sufficient amplification.

The size of the amplified fragments (the "amplification products") produced by the methods of the present invention is typically sufficient to

determine the presence or absence of enteroviruses. Thus, in some embodiments of the invention, size fractionation (e.g., gel electrophoresis) of the amplified fragments produced in a given sample can be used to determine the presence or absence of enteroviruses in the sample. This is typically carried out by amplifying a control containing known nucleic acids with the same primers used to amplify the samples of interest. After running the amplified sequences in an agarose gel and labeling with ethidium bromide according to conventionally known techniques (see, Sambrook *et al.*), the pattern of bands in the sample and control are compared. The presence of different or additional bands in the sample as compared to the control group is an indication of the presence of enteroviruses.

To ascertain the accuracy of results of PCR amplifications, more than one pair of primers can be employed in an amplification process. In the method according to the present invention, pairs of primers that are different with respect to each other may be employed simultaneously or sequentially. In the case where more than one pair of primers according to the present invention is employed simultaneously in an amplification process, a pair of primers may differ from another pair of primers in either the first primer or the second primer, or both of the first and second primers. In another case, if two pairs of primers according to the present invention are employed sequentially in an amplification process, the second pair of primers is capable of being used to amplify a sequence equal to or within the sequence that is supposedly obtainable in the amplification process using the first pair of primers. According to Figure 1, a practitioner can carry out the methods of the present invention by determining with ease more than one pair of primers that is to be employed simultaneously or sequentially.

Alternatively, the amplification products of the present invention can be detected using oligonucleotide probes specific to the target nucleic acids. The probes are usually selected from the regions of the genome of the enterovirus that are specific to one or the other.

Sequence-specific probe hybridization is a well-known method of

detecting desired nucleic acids in a sample. Under sufficiently stringent hybridization conditions, the probes hybridize specifically only to substantially complementary sequences. The stringency of the hybridization conditions can be relaxed to tolerate varying amounts of sequence mismatch.

5 Detection of the amplified product utilizes this sequence-specific hybridization to insure detection of only the correct amplified target, thereby decreasing the chance of a false positive caused by the presence of homologous sequences from related organisms or other contaminating sequences.

10 It is surprisingly found in the present invention that certain nucleotide sequences correspond to the conserved portions in the nucleic acids of the enteroviruses. Therefore, the present invention further provides the synthetic nucleotide sequences capable of specifically hybridizing to a sense strand of an enterovirus nucleic acid or a nucleic acid corresponding to the sense
15 strand (such as the product of an amplification reaction using the sense strand as the template). Those synthetic nucleotide sequences are useful as probes in hybridization assays for enteroviruses. Preferably, the synthetic nucleotide sequences selected from the group consisting of

p1: TCCTCCGGCCCCCTGAATGCGGCTAATC (SEQ ID NO: 9),
p2: TGTCGTAACGSGCAASTCYGYRGC GGAACCGAC (SEQ ID NO: 10),
p3: TACTTTGGGTGTCCGTGTTTCHTTTAT (SEQ ID NO: 11),
71-2: C TTA TAA GCA GAC TCA ACC CGG TGC TGA TG (SEQ ID NO: 12),
71-3: TGG CAT TCC AAT ATC ACA ATT AAC AGT G (SEQ ID NO: 13),
16-1: CTC GGC ACT ATC GCA GGA GGG ACC GGG AAT (SEQ ID NO: 14) and
16-2: C CTA CGC CAC TAC ACA GCC TGG TCA GGT TG (SEQ ID NO: 15).

The synthetic nucleotide sequences of the present invention correspond
20 to the known enteroviral cDNA sequences in the boxes as shown in Figure 1. The nucleotide sequences comprising the sequences of SEQ ID NOs:12-15 according to the present invention correspond to the coding regions of the enteroviral genome. The nucleotide sequences corresponding to the coding regions of the enteroviral genome are intended to cover those comprising the
25 degenerate sequences in relation to the sequences of SEQ ID NOs:12-15.

The sequences of SEQ ID NOs:12-15 above are schematically depicted in relevant triplets according to the codons to which the sequences correspond.

In view of Figure 1, persons skilled in the art can understand the way to choose at least a nucleotide sequence of the present invention for use as a probe in a hybridization assay using the primers of the present invention, and accordingly determine the probe(s) with ease. As shown in Figure 1, the nucleotide sequence should not comprise a sequence of any of SEQ ID Nos:12-15 nor a degenerate sequence thereof when the second primer comprising the sequence of SEQ ID NO:8 or a degenerate sequence thereof is not employed for amplification. Moreover, the nucleotide sequence should not comprise a sequence of any of SEQ ID Nos:9-11 when the first primer comprising the sequence of SEQ ID NO:5 or a degenerate sequence thereof is not employed for amplification.

Several hybridization modes are well known in the art, including but not limited to, solution phase, solid phase, mixed phase or *in situ* hybridization assays. In solution (or liquid) phase hybridizations, both the target nucleic acid and the probe or primer are free to interact in the reaction mixture. In solid phase hybridization assays, either the target or probes are linked to a solid support where they are available for hybridization with complementary nucleic acids in solution. Exemplary solid phase modes include Southern hybridizations, dot blots and the like. The detection for hybridization may be carried out on a solid support such as a microtiter plate, a membrane (e.g. nitrocellulose) or a microsphere (bead) or a chip and any feasible hybridization buffer system.

The hybridization complexes are detected according to well-known techniques, and such detection is not a critical aspect of the present invention. Nucleic acid probes capable of specifically hybridizing to a target can be labeled by any one of several methods typically used to detect the presence of hybridized nucleic acids.

A common method of detection is the use of autoradiography using probes labeled with ^3H , ^{125}I , ^{35}S , ^{14}C , ^{32}P or the like. The choice of

radioactive isotope depends on research preferences due to ease of synthesis, stability and half-life of the selected isotopes. The detection of hybridization signals may be conducted on a solid support, such as a microtiter plate, a membrane (e.g. nitrocellulose), a microsphere (bead) or a chip, as well as any feasible hybridization buffer system.

Other labels include ligands which bind to antiligands or antibodies labeled with fluorophores, chemilluminiscent agents and enzymes. Alternatively, probes can be conjugated directly with labels such as fluorophores, chemiluminescent agents or enzymes. The choice of label depends on sensitivity required, ease of conjugation with the probe, stability requirements and available instrumentation.

The probes and primers of the invention can be synthesized and labeled using conventionally known techniques. Oligonucleotides for use as probes and primers may be chemically synthesized according to the solid phase phosphoramidite triester method first described by Beaucage, S.L. and Caruthers, M.H., 1981, Tetrahedron Letts., 22(20):1859-1862 using an automated synthesizer, as described in Needham-VanDevanter, D.R., *et al.* 1984, Nucleic Acids Res., 12:6159-6168. Purification of oligonucleotides is by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., 1983, J. Chrom., 255:137-149.

The above described primers and assays are used to detect enteroviruses in a sample, to diagnose enteroviral diseases and medical conditions and to correlate (or disprove a correlation between) specific symptoms or combinations of symptoms with the presence of a particular enterovirus. Diagnostic applications are supplemented and confirmed by an examination of the medical history and profile of the individual tested. Enteroviral diseases, medical conditions and symptoms that are diagnosed by the methods of the invention encompass all diseases, medical conditions and symptoms reported to be associated with enteroviruses here and in the scientific literature, specifically including aseptic meningitis, enteroviral

diabetes mellitus, enteroviral conjunctivitis, acute flaccid paralysis, acute benign pericarditis, exanthema, enanthema, dilated cardiomyopathy, foot and mouth disease, chronic fatigue syndrome, febrile illnesses and upper respiratory tract infections. The detection of enteroviral infections and their correlation with medical conditions will make possible vaccines and methods of treatment.

The present invention also provides kits, multicontainer units comprising components useful for practicing the present method. A useful kit can contain probes for detecting the desired target nucleic acid. In some cases, the probes may be fixed to an appropriate support membrane. The kit will also contain primers provided in the present invention. Other optional components of the kit include, for example, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin) and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. In addition to the above components, the kit can also contain instructions for carrying out the method of the present invention.

All of the literature and publications as recited in the context of the present disclosure are incorporated herein by reference.

Other features and advantages of the present invention will be apparent from the following description of the preferred embodiments and from the claims.

Examples

The following examples illustrate various aspects of the present invention but do not limit the claims in any manner whatsoever.

Example 1: Detection of enteroviruses

1.1. Viruses

59 Enteroviral specimens (see Table 1) used were either isolated from samples collected in clinic or obtained from the American Type Culture

Collection (ATCC). The enteroviruses were identified by neutralization assays using pools of immuosera, followed by the confirmation of their serotypes with monotypic neutralizing polyclonal antibodies. As the results indicated, the 59 specimens covers a variety of enteroviral serotypes (see Table 1). Viruses were propagated in MRC5 cell monolayer cultures.

1.2. RNA extraction

Viral RNAs were obtained by the isolation of total nucleic acids from cell pellets of the infected monolayer cell cultures. Approximately $4-6 \times 10^6$ cells per ml were lysed in a lysis buffer (50 mM NaCl, 20mM Tris HCl (pH 7.5), 50 mM EDTA, 1% sodium dodecyl sulfate), extracted three times with phenol-chloroform and once with chloroform and then precipitated from 2.5 M ammonium acetate with ethanol. Nucleic acid pellets were washed with 75% ethanol, dried and suspended in 100 μ l of sterile distilled water. RNA preparations were stored at -80°C .

1.3. PCR amplification assays

The first step of the amplification was the synthesis of a DNA copy (cDNA) of the portion of the enteroviral RNA genome to be amplified (i.e., the reverse transcription step). Reverse transcription by polymerase chain reactions were carried out in 20 μ l of reaction mixtures (1 μ l of each of total RNA in 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 5 mM MgCl_2 , 10 mM DTT, 0.5 mM of each of dATP, dCTP, dGTP and dTTP, and 50 ng of random hexamers). Samples were incubated at 65°C for 5 minutes, then placed on ice for at least 1 minute. 50 units of reverse transcriptase were added and the mixtures were incubated at 42°C for 50 minutes. The reactions were ceased by incubation at 70°C for 15 minutes. The obtained cDNA products were stored at -20°C .

DNA amplifications by PCR were carried out in 25 μ l reaction mixtures [12 μ l of cDNA, 20 mM Tris-HCl (pH 8.0), 0.1 mM EDTA, 1 mM DTT, 1.0% triton X-100, 50% glycerol, 1.5 mM MgCl_2 , 150 μ M of each of dATP, dCTP, dGTP and dTTP, 10 pmol of each primer and 2.5 U of Taq DNA polymerase]. The primer pairs used in the amplification reactions were

those comprising the sequences of

f1(SEQ ID NO: 1)/**r1**(SEQ ID NO: 6), **f2**(SEQ ID NO: 2)/**r1**(SEQ ID NO: 6),
f3(SEQ ID NO: 3)/**r1**(SEQ ID NO: 6); **f5**(SEQ ID NO: 4)/**r1**(SEQ ID NO: 6),
f1(SEQ ID NO: 1)/**r2**(SEQ ID NO: 7), **f2**(SEQ ID NO: 2)/**r2**(SEQ ID NO: 7),
f3(SEQ ID NO: 3)/**r2**(SEQ ID NO: 7) and **f5**(SEQ ID NO: 4)/**r2**(SEQ ID NO: 7).

Primers **r1** and **r2** were labeled with biotin at 5' end for the following detection procedure. Each amplification reaction was conducted for 40 thermal cycles (denaturation for 4 minutes at 94°C, primer annealing for 1 minute at 55°C, and elongation for 1 minute at 72°C).

1.4. Separation of DNA products

Aliquots of PCR products (10 µl for each) were subjected to electrophoresis on 1.5% agarose gel in 0.5x TBE buffer (0.045M Tris-borate, 0.001M EDTA) for 30 minutes at 100 volts. After electrophoresis, the gel was stained with ethidium bromide and observed under UV illumination. The amplifications of all viral specimens using the primers of the present invention showed positive results by observation under UV. The data of the PCR amplification using the primer pair **f5/r1** for the 59 viral specimens are illustrated in Table 1.

Table 1

Serotype	Case No.	Case No. showing positive PCR results
EV 71	17	17
CA 7	2	2
CA 9	1	1
CA 10	1	1
CA 11	1	1
CA 16	14	14
CA 24	1	1
CB 1	1	1
CB 2	1	1

CB 3	1	1
CB 4	1	1
CB 5	5	5
CB 6	1	1
Echo 1	1	1
Echo 2	1	1
Echo 3	1	1
Echo 4	1	1
Echo 5	1	1
Echo 6	1	1
Echo 7	3	3
Echo 9	1	1
Echo 11	1	1
Echo 14	1	1
Total	59	59

1.5. Hybridization analysis

Three enterovirus-specific probes (**p1**, **p2** and **p3**) were used to detect the amplified DNA fragments, which comprise the sequences of SEQ ID NO: 9, SEQ ID NO: 10 and SEQ ID NO: 11, respectively.

The probes were denatured by heat (95°C, 5 minutes) and quickly quenching on ice for 2 minutes, followed by immobilization of those probes (10µM for each) on nylon membranes (available from Boehringer Manngem). The three probes (one µl for each) were applied and exposed to a source of ultraviolet irradiation (254nm, 0.15 J/cm²).

Biotin-labeled PCR products (8 µl for each) were denatured by heating at 95°C for 5 minutes and then quenched on ice for 2 minutes, and were added into a hybridization solution [5x standard saline citrate (SSC), 0.1% (w/v) N-lauroylsarcosine, 0.1% (w/v) sodium dodecyl sulfate (SDS), 1 x blocking buffer (Boehringer Manngem) (20 ml/100 cm²)]. The hybridization solution containing the PCR products was then incubated with the nylon membranes bound with labeled probes. After incubation at 50°C

for 1 hour, the membranes were washed 5 times at room temperature by a washing buffer (2 x SSC of 0.1% SDS), followed by the addition of streptavidin alkaline phosphatase (2 µl/20 ml 1 x blocking solution). The membranes were placed at room temperature for 30 minutes and then washed five times at room temperature with a maleic acid buffer (0.1 M maleic acid, 0.15 M NaCl, pH 7.5). The membranes were then equilibrated in a detection buffer (0.1 M Tris-HCl; 0.1 M NaCl; 50 mM MgCl₂, pH 9.5) for 5 minutes and incubated with a freshly prepared color-substrate solution (45 µl NBT solution mixed with 35 µl X-phosphate solution, and the detection buffer was added to 10 ml) in the dark for 10 minutes. Finally the membrane were washed with 1x TE buffer solution to stop reaction and air-dried at room temperature. The hybridization signals were detected and recorded. The results are shown in Table 2.

Table 2

Serotype	Number of test cases	Number of cases showing detectable hybridization signals		
		P1	P2	P3
CA 16	6	6	6	6
CA 21	1	1	1	1
CA 24	1	1	1	1
CB 1	1	1	1	1
CB 2	2	2	2	2
CB 3	1	1	1	1
CB 4	1	1	1	1
CB 5	1	1	1	1
CB 6	1	1	1	1
Echo 3	3	3	3	3
Echo 5	1	1	1	1
Echo 6	1	1	1	1
Echo 9	2	2	2	2
Echo 11	3	3	3	3
Echo 14	1	1	1	1
Echo 21	3	3	3	3
Echo 24	1	1	1	1

Echo 30	2	2	2	2
Echo 31	2	2	2	2
EV 71	7	7	7	7
Polio 1	2	2	2	2
Polio 2	2	2	2	2
Polio 3	2	2	2	2

Example 2: Detection and differentiation of enterovirus type 71 (EV71) and coxsackievirus A16 (Cox A16)

2.1. PCR amplification assay:

RNA extraction and reverse transcription were carried out in the same conditions described in Example 1. PCR primers used in the assay were those comprising the sequences of f7 (SEQ ID NO: 5)/ r4 (SEQ ID NO: 8).

The PCR reaction mixtures and thermal cycling conditions were adjusted as described in Example 1.

2.2. Hybridization assay:

The probes used for the detection of EV 71 were those comprising the sequences of SEQ ID NO: 12 (71-2) and SEQ ID NO: 13 (71-3). The probes used in the Cox A16 detection assay were those comprising the sequences of SEQ ID NO: 14 (16-1) and SEQ ID NO: 15 (16-2). Hybridization assays were performed in the conditions described in Example 1.

Results showed that the method of the present invention using primer pair f7/r4 and the probes 71-2 and 71-3 could specifically detect and differentiate EV71 and non-EV71 enteroviruses. Results also showed that the method of the present invention using the primer pair f7/r4 and the probes 16-1 and 16-2 could specifically detect and differentiate Cox A16 and non-Cox A16 enteroviruses.

Example 3: Kit for detecting and differentiating EV71, Cox A16, non-EV71 enteroviruses and non-Cox A16 enteroviruses

EV71 and Cox A16 were subjected to a detection assay simultaneously using a kit of the present invention. The kit provides materials and protocols to enable a practitioner to conduct a multiplex PCR assay. Viral RNA extraction and reverse transcription were carried out as described in Example

1. The multiplex PCR were carried out in 25 µl reaction mixtures (each containing 12 µl of cDNA, 50 mM Tris-HCl (pH 8.3), 70 mM KCl, 2.5 mM MgCl₂, 200 µM of each of dATP, dCTP, dGTP and dTTP, 10 pmol of the primers **f5/r1**, 20 pmol of the primers **f7/r4** and 3 U of Taq DNA polymerase). Amplifications were conducted in 40 thermal cycles consisting of denaturation for 4 minute at 94°C, primer annealing for 1 minute at 55°C, and elongation for 1 minute at 72°C. After the multiplex PCR amplifications, the PCR products obtained were incubated with a membrane immobilized with the probes (**p1**, **p2** and **p3** for enteroviruses, **71-2** and **71-3** specific for EV71, and **16-1** and **16-2** specific for Cox A16). All conditions of the hybridization assay were the same as those described in Example 1. Results show that the kit providing a system comprising multiplex PCR and multiplex hybridization detection could both detect and differentiate EV71, Cox A16, non-EV71 enteroviruses and non-Cox A16 enteroviruses. The data of the hybridization assay using different probes of the present invention are illustrated in Table 3.

Table 3

Serotype of enterovirus	Number of test cases	Number of cases showing detectable hybridization signals						
		probes of the present invention						
		p1	p2	p3	71-2	71-3	16-1	16-2
CA 16	6	6	6	6	0	0	6	6
CA 21	1	1	1	1	0	0	0	0
CA 24	1	1	1	1	0	0	0	0
CB 1	1	1	1	1	0	0	0	0
CB 2	2	2	2	2	0	0	0	0
CB 3	1	1	1	1	0	0	0	0
CB 4	1	1	1	1	0	0	0	0
CB 5	1	1	1	1	0	0	0	0
CB 6	1	1	1	1	0	0	0	0
Echo 3	3	3	3	3	0	0	0	0
Echo 5	1	1	1	1	0	0	0	0
Echo 6	1	1	1	1	0	0	0	0

Echo 9	2	2	2	2	0	0	0	0
Echo 11	3	3	3	3	0	0	0	0
Echo 14	1	1	1	1	0	0	0	0
Echo 21	3	3	3	3	0	0	0	0
Echo 24	1	1	1	1	0	0	0	0
Echo 30	2	2	2	2	0	0	0	0
Echo 31	2	2	2	2	0	0	0	0
EV 71	7	7	7	7	7	7	0	0
Polio 1	2	2	2	2	0	0	0	0
Polio 2	2	2	2	2	0	0	0	0
Polio 3	2	2	2	2	0	0	0	0

Various modifications and variations of the present invention will be apparent to those persons skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in the art are intended to be within the scope of the following claims.

We claim

1. A pair of oligonucleotide primers for use in detecting the presence or absence of an enterovirus in a sample, wherein a first primer of said pair
5 comprises a sequence of any of:

SEQ ID NO: 1: TTGTRCGCCTGTTTTA,

SEQ ID NO: 2: CAAGCACTTCTGTHHCCCCGG,

SEQ ID NO: 3: TACTTCGAGAARCCYAGTA,

SEQ ID NO: 4: AAGAGYCTATTGAGCTA, or

10 SEQ ID NO: 5: GGITGGTRSTGGAARTTICC, or a degenerate sequence of SEQ ID No: 5; and

a second primer of said pair comprises a sequence of any of:

SEQ ID NO: 6: CACYGGATGGCCAATCCAA,

SEQ ID NO: 7: ATTGTCACCATAAGCAGCCA, or

15 SEQ ID NO: 8: ARRTTIATCCAYTGRTGIGG, or a degenerate sequence of SEQ ID No: 8,

provided that the second primer comprises the sequence of SEQ ID NO: 8 or a degenerate sequence thereof when the first primer comprises the sequence of SEQ ID NO: 5 or a degenerate sequence thereof.

20 2. A pair of primers according to claim 1, which comprises a sequence selected from the group consisting of: SEQ ID NO: 1/SEQ ID NO: 6; SEQ ID NO: 2/SEQ ID NO: 6; SEQ ID NO: 3/SEQ ID NO: 6; SEQ ID NO: 4/SEQ ID NO: 6; SEQ ID NO: 1/SEQ ID NO: 7; SEQ ID NO: 2/SEQ ID NO: 7; SEQ ID NO: 3/SEQ ID NO: 7; SEQ ID NO: 4/SEQ ID NO: 7; and SEQ ID
25 NO: 5/SEQ ID NO: 8.

3. A pair of primers according to claim 1, which is SEQ ID NO: 5/SEQ ID NO: 8.

4. A pair of primers according to claim 3 for use in the detection of enterovirus type 71 (EV71) or coxsackievirus A16 (Cox A 16).

30 5. A synthetic nucleotide sequence comprising any selected from the group consisting of:

SEQ ID NO:9: TCCTCCGGCCCCTGAATGCGGCTAATC,

SEQ ID NO:10: TGTCGTAACGSGCAASTCYGYRGCGGAACCGAC,

SEQ ID NO:11: TACTTTGGGTGTCCGTGTTTCHTTTTAT,

SEQ ID NO:12: CTTATAAGCAGACTCAACCCGGTGCTGATG,

SEQ ID NO:13: TGGCATTCCAATATCACAATTAACAGTG,

5 SEQ ID NO:14: CTCGGCACTATCGCAGGAGGGACCGGGAAT and

SEQ ID NO:15: CCTACGCCACTACACAGCCTGGTCAGGTTG, and a
degenerate sequence of any of SEQ ID Nos: 12-15,

which is capable of specifically hybridizing to a sense strand of an
enterovirus nucleic acid or a nucleic acid corresponding to the sense strand.

10 6. A method of detecting the presence or absence of an enterovirus
nucleic acid in a sample, which comprises the following steps:

(a) contacting the sample with a pair of oligonucleotide primers
according to claim 1 in an amplification process; and

15 (b) determining the presence or absence of an enterovirus by
detecting for the presence or absence of amplification products.

7. A method according to claim 6, wherein in step (a) the sample is
simultaneously contacted with a second pair of the oligonucleotide primers
according to claim 1 in an amplification process, and the second pair of
primers are not the same as the first pair of primers.

20 8. A method according to claim 6, wherein the first primer in the second
pair is different from the first primer in the first pair.

9. A method according to claim 6, wherein the second primer in the
second pair is different from the second primer in the first pair.

25 10. A method according to claim 7, wherein the primers in the second pair
are different from the primers in the first pair.

11. A method according to claim 7, wherein in step (a) the sample is
simultaneously contacted with a third pair of the oligonucleotide primers
according to claim 1 in an amplification process, and the third pair of primers
are not the same as either the first pair of primers or the second pair of
30 primers.

12. A method according to claim 6, which further comprises contacting
the products of step (a) with a second pair of the oligonucleotide primers

according to claim 1 in an amplification process, wherein the second pair of primers is capable of being used to amplify a sequence equal to or within the sequence obtainable in the amplification process using the first pair of primers.

5 13. A method according to claim 6, wherein the amplification products detected are further subjected to a specific hybridization with at least one synthetic nucleotide sequence according to claim 5, provided that the nucleotide sequence does not comprise a sequence of any of SEQ ID Nos:12-15 nor a degenerate sequence thereof when the second
10 primer comprising the sequence of SEQ ID NO:8 or a degenerate sequence thereof is not employed for amplification, and that the nucleotide sequence does not comprise a sequence of any of SEQ ID Nos:9-11 when the first primer comprising the sequence of SEQ ID NO:5 or a degenerate sequence thereof is not employed for amplification.

15 14. A method according to claim 13, wherein the hybridization is conducted under highly stringent conditions.

15. A method of detecting and differentiating enterovirus type 71 in a sample, which comprises:

(a) contacting the sample with at least one pair of oligonucleotide
20 primers according to claim 1 in an amplification process, provided that the second primer comprises the sequence of SEQ ID NO:8 or a degenerate sequence thereof;

(b) determining the presence or absence of enterovirus type 71 by detecting for the presence or absence of amplification products; and

25 (c) subjecting the amplification products detected to a specific hybridization with at least one synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13.

16. A method according to claim 15, wherein in step (c) the amplification products are subjected to a specific hybridization with the synthetic
30 nucleotide sequences comprising the sequences of SEQ ID NO:12 and SEQ ID NO:13.

17. A method of detecting and differentiating coxsackievirus A16 in a sample, which comprises the following steps:

(a) contacting the sample with at least one pair of oligonucleotide primers according to claim 1 in an amplification process, provided that the second primer comprises the sequence of SEQ ID NO:8 or a degenerate sequence thereof;

(b) determining the presence or absence of coxsackievirus A16 by detecting for the presence or absence of amplification products; and

(c) subjecting the amplification products detected to a specific hybridization with at least one synthetic nucleotide sequence comprising the sequence of SEQ ID NO:14 or SEQ ID NO:15.

18. A method according to claim 17, wherein in step (c) the amplification products are subjected to a specific hybridization with the synthetic nucleotide sequences comprising the sequences of SEQ ID NO:14 and SEQ ID NO:15.

19. A method of detecting and differentiating enterovirus type 71 and/or coxsackievirus A16 in a sample, which comprises:

(a) contacting the sample with at least one pair of oligonucleotide primers according to claim 1 in an amplification process, provided that the second primer comprises the sequence of SEQ ID NO:8 or a degenerate sequence thereof;

(b) determining the presence or absence of enterovirus type 71 and/or coxsackievirus A16 by detecting for the presence or absence of amplification products; and

(c) subjecting the amplification products detected to a specific hybridization with at least a first synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13, and with at least a second synthetic nucleotide sequence comprising the sequence of SEQ ID NO:14 or SEQ ID NO:15.

20. A method according to claim 19, wherein in step (c) the amplification products are subjected to a specific hybridization with the synthetic

nucleotide sequences comprising the sequences of SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14 and SEQ ID NO:15.

21. A kit for detecting an enterovirus in a sample, which comprises at least one pair of oligonucleotide primers according to claim 1, provided that the second primer comprises the sequence of SEQ ID NO: 8 or a degenerate sequence thereof when the first primer comprises the sequence of SEQ ID NO: 5 or a degenerate sequence thereof.

22. A kit according to claim 21, which comprises more than one pair of oligonucleotide primers according to claim 1.

23. A kit according to claim 22, which further comprises at least one synthetic nucleotide sequence according to claim 5, provided that the nucleotide sequence does not comprise a sequence of any of SEQ ID Nos:12-15 nor a degenerate sequence thereof when the second primer comprising the sequence of SEQ ID NO:8 or a degenerate sequence thereof is not employed for amplification, and that the nucleotide sequence does not comprise a sequence of any of SEQ ID Nos:9-11 when the first primer comprising the sequence of SEQ ID NO:5 or a degenerate sequence thereof is not employed for amplification.

24. A kit for detecting and differentiating enterovirus type 71 in a sample, which comprises at least one pair of oligonucleotide primers according to claim 1, provided that the second primer comprises the sequence of SEQ ID NO:8 or a degenerate sequence thereof; and at least one synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13.

25. A kit for detecting and differentiating coxsackievirus A16 in a sample, which comprises:

at least one pair of oligonucleotide primers according to claim 1, provided that the second primer comprises the sequence of SEQ ID NO:8 or a degenerate sequence thereof; and

at least one synthetic nucleotide sequence comprising the sequence of SEQ

ID NO:14 or SEQ ID NO:15.

26. A kit for detecting and differentiating enterovirus type 71 and/or coxsackievirus A16 in a sample, which comprises:

at least one pair of oligonucleotide primers according to claim 1, provided
5 that the second primer comprises the sequence of SEQ ID NO:8 or a degenerate sequence thereof; and

at least a first synthetic nucleotide sequence comprising the sequence of SEQ ID NO:12 or SEQ ID NO:13 and at least a second synthetic nucleotide sequence comprising the sequence of SEQ ID NO:14 or SEQ ID NO:15.

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Abstract of the Disclosure

The present invention discloses pairs of oligonucleotide primers for use in detecting the presence or absence of an enterovirus in a sample. Also disclosed are synthetic nucleotide sequences capable of specifically hybridizing to a sense strand of an enterovirus nucleic acid or a nucleic acid corresponding to the sense strand. The present invention provides a method of detecting the presence or absence of an enterovirus nucleic acid in a sample as well as a kit for detecting an enterovirus in a sample. The present invention particularly provides a method and a kit for detecting and differentiating enterovirus type 71 and/or coxsackievirus A16 in a sample.

**Nucleotides 1-1560 of the genome of
Enterovirus type 71 BrCr (GenBank Accession No.: U22521)**

1 TTAAACAGC TGTGGGTTGT CACCCACCCA CAGGGTCCAC TGGGCGCTAG TACACTGGTA
61 TCTCGGTACC TTTGTACGCC TGTTTTATAC CCCCTCCCTG ATTTGCAACT TAGAAGCAAC

f1 (72-87)

121 GCAAACCAGA TCAATAGTAG GTGTGACATA CCAGTCGCAT CTTGATCAAG CACTTCTGTA

181 TCCCCGGACC GAGTATCAAT AGACTGTGCA CACGGTTGAA GGAGAAAACG TCCGTTACCC

f2 (167-187)

241 GGCTAACCTAC TTCGAGAAGC CTAGTAACGC CATTGAAGTT GCAGAGTGTT TCGCTCAGCA

f3 (248-266)

301 CTCCCCCGGT GTAGATCAGG TCGATGAGTC ACCGCATTCC CCACGGGCGA CCGTGGCGGT
361 GGCTGCGTTG GCGGCCTGCC TATGGGGTAA CCCATAGGAC GCTCTAATAC GGACATGGCG
421 TGAAGAGTCT ATTGAGCTAG TTAGTAGTCC TCCGCCCCCT GAATGCGGCT AATCCTAACT

f5 (423-439) **p1 (448-474)**

481 GCGGAGCACA TACCCTTAAT CCAAAGGGCA GTGTGTCGTA ACGGGCAACT CTGCAGCGGA

p2 (514-546)

541 ACCGACTACT TTGGGTGTCC GTGTTTCTTT TTATCTTTGT ATTTGGCTGCT TATGGTGACA

p3 (547-574) **r2 (583-602)**

601 ATTAAAGAAT TGTTACCATA TAGCTATTGG ATTGGCCATC CAGTGTCAAA CAGAGCTATT

r2 (583-602) **r1 (627-645)**

661 GTATATCTCT TTGTTGGATT CACACCTCTC ACTCTTGAAA CGTTACACAC CCTCAATTAC
721 ATTATACTGC TGAACACGAA GCGATGGGCT CCCAGGTCTC CACACAGCGA TCCGGCTCGC
781 ATGAGAATTC CAACTCAGCC ACGGAAGGCT CCACTATAAA TTACACAACC ATTAATTACT
841 ACAAAGACTC GTATGCTGCC ACTGCTGGAA AGCAAAGTCT CAAACAAGAT CCTGACAAGT
901 TTGCGAACCC TGTGAAGGAC ATCTTTACTG AAATGGCAGC GCCCTTAAAG TCTCCCTCTG
961 CTGAAGCATG TGGCTATAGC GACCGAGTGG CACAGCTTAC CATTGGAAAT TCCACCATTA
1021 CTACACAAGA AGCAGCAAAC ATAATAGTTG GGTATGGTGA GTGGCCTTCA TACTGCTCTG
1081 ATAATGATGC AACAGCGGTA GACAAACCTA CACGGCCTGA TGTCTCAGTA AATAGATTTT
1141 ACACGCTAGA CACTAAGCTA TGGGAGAAAT CATCCAAGGG GTGGTACTGG AAGTTCCCAG

f7 (1179-1198)

1201 ATGTA CTGAC TGAAACCGGA GTTTTTGGTC CAAATGCACA ATTTCACTAC TTATACCGTT
1261 CAGGGTTCTG CATCCACGTT CAATGTAACG CTAGCAAATT TCACCAAGGG GCGCTACTCG
1321 TTGCGGTATT GCCCGAGTAT GTCATTGGAA CAGTGGCAGG CGGCACAGGC ACAGAGAACA

16-1 (1343-1373)

1381 GTCACCCTCC TTATAAACAA ACCCAACCCG GCGCTGATGG ATTTGAATTA CAACATCCAT

71-2 (1390-1419)/16-2 (1390-1419)

1441 ATGTTCTTGA TGTGGAATT CCAATATCTC AGTTGACAGT GTGCCTCAC CAGTGGATCA

71-3 (1453-1481) **r4 (1485-1504)**

1501 ATTTACGAAC CAACAATTGT GCCACCATAA TAGTGCCATA CATGAACACA CTACCTTTTG

Figure 1

DECLARATION FOR PATENT APPLICATION AND APPOINTMENT OF ATTORNEY

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name; I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention (Design, if applicable) entitled: Method for Detecting and Differentiating Enteroviruses and the Primers and Probes Therefor

the specification of which (check one):

☒ is attached hereto.

☐ was filed on:

as Application Serial No.:

and (if applicable) was amended on:

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment(s) referred to above. I acknowledge the duty to disclose information which is material to patentability as defined in **Title 37, Code of Federal Regulations, § 1.56**. I hereby claim foreign priority benefits under **Title 35, United States Code § 119** of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN APPLICATION(S)			PRIORITY CLAIMED	
Number	Country	Day/Month/Year Filed	Yes	No

I hereby claim the benefit under **Title 35, United States Code, § 120** of any United States application(s) or PCT international application(s) designating The United States of America listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in that/those prior application(s) in the manner provided by the first paragraph of **Title 35, United States Code, § 112**, I acknowledge the duty to disclose information which is material to patentability as defined in **Title 37, Code of Federal Regulations, § 1.56** which became available between the filing date of the prior application(s) and the national or PCT international filing date of this application:

Application Number	Filing Date	Status - Patented, Pending or Abandoned

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under **section 1001 of title 18 of the United States Code** and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: I(We) hereby appoint as my(our) attorneys, with full powers of substitution and revocation, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith:
 Stephen F. Gass 38,462; Charles H. DeVoe 37,305; David S. D'Ascenzo 39,952; Owen W. Dukelow 41,002; James R. Abney 42,253; Mark D. Alleman 42,257; J. David Fulmer 42,561; M. Matthews Hall 43,653; Christopher S. Tuttle 41,357

I(We) authorize my(our) attorneys to accept and follow instructions from **TAI E INTERNATIONAL PATENT & LAW OFFICE** regarding any matter related to the preparation, examination, grant and maintenance of this application, any continuation, continuation-in-part or divisional based thereon, and any patent resulting therefrom, until I(We) or my(our) assigns withdraw this authorization in writing.

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Telephone Calls to: 503-224-6655

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Full Name of First or Sole Inventor Kan-Hung LEE	
Post Office Address <input checked="" type="checkbox"/> Same as Residence	Citizenship Taiwan, R.O.C.
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DATE November 22, 2000	SIGNATURE <i>Kan-Hung Lee</i>
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DATE November 22, 2000	SIGNATURE <i>Chi-Horng Bair</i>

☐ See following pages for additional joint inventors.

DECLARATION FOR PATENT APPLICATION AND APPOINTMENT OF ATTORNEY

Page 2

Full Name of Joint Inventor Yang-Yuan TSENG	Citizenship Taiwan, R.O.C.
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DATE November 22, 2000	SIGNATURE <i>Yang-Yuan Tseng</i>

Full Name of Joint Inventor Yih-Weng WANG	Citizenship Taiwan, R.O.C.
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DATE November 22, 2000	SIGNATURE <i>Yih-Weng Wang</i>

Full Name of Joint Inventor Shin-Hwan WANG	Citizenship Taiwan, R.O.C.
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DATE November 22, 2000	SIGNATURE <i>Shin-Hwan Wang</i>

Full Name of Joint Inventor	Citizenship
Residence Address	Post Office Address <input type="checkbox"/> Same as Residence
DATE	SIGNATURE

Full Name of Joint Inventor	Citizenship
Residence Address	Post Office Address <input type="checkbox"/> Same as Residence
DATE	SIGNATURE

Full Name of Joint Inventor	Citizenship
Residence Address	Post Office Address <input type="checkbox"/> Same as Residence
DATE	SIGNATURE

POWER OF ATTORNEY

Docket No. TAI 3L6

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of

Inventor(s): Kan-Hung LEE, Chi-Horng BAIR, Yang-Yuan TSENG, Yih-Weng WANG
& Shin-Hwan WANG

Title: Method for Detecting and Differentiating Enteroviruses and the Primers
and Probes Therefor

POWER OF ATTORNEY

Hon. Commissioner of Patents and Trademarks

Washington, D.C. 20231

Sir:

DR. Chip Biotechnology Incorporation

having become the owner of all rights in and to the above-identified application by virtue of an Assignment executed by the inventor(s) concurrently with the execution of the application, said Assignment being submitted herewith for recording, hereby appoints:

Stephen F. Gass 38,462; Charles H. DeVoe 37,305; David S. D'Ascenzo 39,952; Owen W. Dukelow 41,002; James R. Abney 42,253; Mark D. Alleman 42,257; J. David Fulmer 42,561; M. Matthews Hall 43,653; Christopher S. Tuttle 41,357

Whose address is: Kolisch, Hartwell, Dickinson,
McCormack & Heuser
520 S.W. Yamhill Street
Suite 200, Portland,
OR 97204-1378, U.S.A.

their attorneys to prosecute said application and to transact in connection therewith all business in the Patent and Trademark office and before competent International Authorities.

Date: November 22, 2000

Yang Wen-Tung
Legal Representative: Wen-Tung YANG

SEQUENCE LISTING

(1) GENERAL INFORMATION

5 (i) APPLICANTS: Kang-Hung Lee
Chi-Horng Bair
Yang-Yuan Tseng
Yih-Weng Wang
Shing-Hwan Wang

10 (ii) TITLE OF THE INVENTION: METHODS FOR DETECTING AND
DIFFERENTIATING ENTEROVIRUSES AND THE PRIMERS AND PROBES
THEREFOR

15 (iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:
20 (A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM:
(D) SOFTWARE:

30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: -Nov-2000

35 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER:

45 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE:
(B) TELEFAX:
(C) TELEX:

50 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1560 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double strand
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) Original Source:
60 (A) Organism: enterovirus enterovirus type 71 (BrCr)

(IX) Feature:
(A) NAME/KEY:

(B) LOCATION:1..1560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5

ttaaaacagc	tgtgggttgt	cacccaccca	Caggggccac	tgggcgctag	tacactggta	60
tctcgggtacc	tttgtacgcc	tgttttatac	Cccctccctg	atttgcaact	tagaagcaac	120
gcaaaccaga	tcaatagtag	gtgtgacata	Ccagtcgcat	cttgatcaag	cacttctgta	180
tccccggacc	gagtatcaat	agactgtgca	cacggttgaa	ggagaaaacg	tccgttacc	240
ggctaactac	ttcgagaagc	ctagtaacgc	cattgaagtt	gcagagtgtt	tcgctcagca	300
ctccccccgt	gtagatcagg	tcgatgagtc	accgcattcc	ccacgggcga	ccgtggcggt	360
ggctgcgttg	gcggcctgcc	tatggggtaa	cccataggac	gctctaatac	ggacatggcg	420
tgaagagtct	attgagctag	ttagtagtcc	tccggcccct	gaatgcggct	aatcctaact	480
gcggagcaca	tacccttaat	ccaaagggca	gtgtgtcgta	acgggcaact	ctgcagcgga	540
accgactact	ttgggtgtcc	gtgtttcttt	ttattcttgt	attggctgct	tatggtgaca	600
attaaagaat	tgttaccata	tagctattgg	attggccatc	cagtgtcaaa	cagagctatt	660
gtatatctct	ttggttgatt	cacacctctc	actcttgaaa	cgttacacac	cctcaattac	720
attatactgc	tgaacacgaa	gcgatgggct	cccaggtctc	cacacagcga	tccggctcgc	780
atgagaattc	caactcagcc	acggaaggct	ccactataaa	ttacacaacc	attaattact	840
acaaagactc	gtatgctgcc	actgctggaa	agcaaagtct	caaa a aagat	cctgacaagt	900
ttgcgaaccc	tgtgaaggac	atctttactg	aaatggcagc	gcccttaaag	tctccctctg	960
ctgaagcatg	tggctatagc	gaccgagtgg	cacagcttac	cattggaaat	tccaccatta	1020
ctacacaaga	agcagcaaac	ataatagttg	ggtatggtga	gtggccttca	tactgctctg	1080
ataatgatgc	aacagcggta	gacaaaccta	cacggcctga	tgtctcagta	aatagatttt	1140
acacgctaga	cactaagcta	tgggagaaat	catccaaggg	gtggtactgg	aagttcccag	1200
atgtactgac	tgaaaccgga	gttttttggtc	caaatgcaca	atttcactac	ttataaccgtt	1260
cagggttctg	catccacgtt	caatgtaacg	ctagcaaatt	tcaccaaggg	gcgctactcg	1320
ttgcggtatt	gcccagagtat	gtcattggaa	cagtggcagg	cggcacaggg	acagagaaca	1380
gtcaccctcc	ttataaacia	acccaacccg	gcgctgatgg	atttgaatta	caacatccat	1440
atgttcttga	tgctggaatt	ccaatatctc	agttgacagt	gtgccctcac	cagtggatca	1500
atttacgaac	caacaattgt	gccaccataa	tagtgccata	catgaacaca	ctaccttttg	1560

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 16 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ttgtrcgcct gtttta 16

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

caagcacttc tgthccccg g 21

35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

tacttcgaga arccyagta

19

10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 17 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

aagagcyctat tgagcta

17

25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ggitggtrst ggaartticc

20

40

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 19 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

cacyggatgg ccaatccaa

19

(2) INFORMATION FOR SEQ ID NO:8:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

attgtcacca taagcagcca

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

arrttiatcc aytgrtgigg

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

tcctccggcc cctgaatgcg gctaatac

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

tgtcgtaacg sgcaastcyg yrgcggaacc gac

33

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

tactttgggt gtccgtgttt chttttat

28

5 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

cttataagca gactcaaccc ggtgctgatg

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

tggcattcca atatcacaat taacagtg

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ctcggcacta tcgcaggagg gaccgggaat

30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

cctacgccac tacacagcct ggtcagggtg

30